SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:

        (A) NAME: NESTEC S.A

        (B) STREET: AVENUE NESTLE 55,

        (C) CITY: VEVEY

        (D) STATE OR PROVINCE: VAUD

        (E) COUNTRY: SWITZERLAND

        (F) POST CODE: 1800

        (G) TELEPHONE: 021 924 26 09

        (H) FAX: 021 924 28 80

    (ii) TITLE OF THE INVENTION: COFFEE MANNANASE

    (iii) NUMBER OF SEQUENCES: 7

    (iv) COMPUTER READABLE FORM

        (A) MEDIUM TYPE: Floppy disk

        (B) COMPUTER: IBM PC compatible

        (C) OPERATING SYSTEM: PC-DOS/MS-DOS

        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1613 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
TTCATTAAAA ATGGCCTTCT CCAGGAGAAG CAATATCAGC AACTTCTCTT GCTGCTTCCT      60
TGTGATCATC GTCTTATCCC TGCATTGCGA AAATCATATA GTTTCTTCTT CTGCTTCGCG     120
CTTTATTCAA ACAAGAGGAA CCCGATTCGT GTTAGGTGGC TACCCATTTT TTTTCAATGG     180
GTTCAACTCC TACTGGATGA TGCATGTTGC AGCTGAGCCA AGTGAAAGGC ATAAAATTTC     240
CAATGTATTT CGCGAGGCTG CTGCTACAGG GCTTACTGTT TGCCGGACAT GGGCATTCAG     300
CGATGGTGGC GATCGAGCTC TTCAAATGTC CCCCGGAGTC TATGATGAAC GTGTCTTTCA     360
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```
GGCCCTTGAT TTTGTGGTAT CGGAAGCAAG GAAGTATGGA GTTCACTTAA TCCTGAGTCT    420

GACCAACAAC TACAAGGACT TTGGAGGAAG GACGCAATAC GTGACGTGGG CTAAAAATGC    480

CGGAGTACAA GTGAATAGCG ATGATGATTT TTACACCAAG AATGCTGTCA AGGGATATTA    540

CAAGAATCAC ATTAAGAAAG TGTTGACTAG GATCAACACA ATCAGTAGAG TTGCATATAA    600

AGATGATCCA ACAGTCATGG CATGGGAGCT AATAAATGAA CCTCGTTGCC AGGTCGACTT    660

CTCCGGAAAA ACCTTAAATG CTTGGGTTCA AGAAATGGCA ACTTACGTCA AATCACTCGA    720

TAACAAACAC CTTCTAGAAA TAGGCATGGA GGGATTCTAC GGAGATTCAA TGCCAGGCAA    780

AAAGCAGTAC AATCCTGGAT ACCAAGTGGG CACAGATTTT ATCACCAATA ATCTTATCAA    840

AGAGATAGAT TTTGCAACCA TTCATGCATA TCCCGATATT TGGCTGTCTG GACAGAGCGA    900

CGGTGCACAG ATGATGTTCA TGAGAAGGTG GATGACCAGT CACTCCACAG ACTCTAAGAC    960

CATACTTAAA AAACCATTGG TTCTCGCTGA ATTTGGGAAA TCAAGTAAAG ATCCAGGATA    1020

CAGTTTATAT GCCAGGGAGT CATTCATGGC CGCAATTTAC GGTGATATCT ACAGGTTTGC    1080

TAGAAGAGGA GGCATTGCAG GTGGATTGGT TTGGCAAATC CTGGCCGAGG GAATGCAACC    1140

GTACGCAGAT GGGTATGAAA TTGTCTTGTC TCAGAACCCA TCAACCGGAC GAATCATAAG    1200

CCAACAGTCT CGACAAATGA CTTCACTCGA CCATATGAGC AGTAATAGAA CCAATTCTCA    1260

AAGCAACAAA CTGCGCAATT CAAAGGAGCA GTGATCAGTC TTCCAGAAAG TCTACTTGAG    1320

TTTGTTCGTA TGTCAAAATC AAGTATCAAC CATAGAAATT TCCATTATAT TCGGAGTGTT    1380

TTAGTCAAGT TCTAGTAATA CCGCTGGAGT CATGATAGTT ATGACAGTAA TACCGCTGGA    1440

GTCAAGTTCT AGTAATACCG TTGGAGTCAA GTTATGATAG TTATTTAAAA ATTAGTATTT    1500

TATTACAAAT TTGTTATTGT TGTGAGACTT GTTTATTAAG TAAATGGAAA GTCTTATCAT    1560

TATTATCATT TGAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA          1613
```

(2) INFORMATION FOR SEQ ID NO: 2:

     (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 427 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: [lacuna]

        (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Phe Ser Arg Arg Ser Asn Ile Ser Asn Phe Ser Cys Cys Phe
1               5                   10                  15

Leu Val Ile Ile Val Leu Ser Leu His Cys Glu Asn His Ile Val Ser
                20                  25                  30

Ser Ser Ala Ser Arg Phe Ile Gln Thr Arg Gly Thr Arg Phe Val Leu
        35                  40                  45
```

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```
Gly Gly Tyr Pro Phe Phe Phe Asn Gly Phe Asn Ser Tyr Trp Met Met
    50                  55                  60

His Val Ala Ala Glu Pro Ser Glu Arg His Lys Ile Ser Asn Val Phe
65                  70                  75                  80

Arg Glu Ala Ala Ala Thr Gly Leu Thr Val Cys Arg Thr Trp Ala Phe
                85                  90                  95

Ser Asp Gly Gly Asp Arg Ala Leu Gln Met Ser Pro Gly Val Tyr Asp
                100                 105                 110

Glu Arg Val Phe Gln Ala Leu Asp Phe Val Val Ser Glu Ala Arg Lys
            115                 120                 125

Tyr Gly Val His Leu Ile Leu Ser Leu Thr Asn Asn Tyr Lys Asp Phe
        130                 135                 140

Gly Gly Arg Thr Gln Tyr Val Thr Trp Ala Lys Asn Ala Gly Val Gln
145                 150                 155                 160

Val Asn Ser Asp Asp Asp Phe Tyr Thr Lys Asn Ala Val Lys Gly Tyr
                165                 170                 175

Tyr Lys Asn His Ile Lys Lys Val Leu Thr Arg Ile Asn Thr Ile Ser
                180                 185                 190

Arg Val Ala Tyr Lys Asp Asp Pro Thr Val Met Ala Trp Glu Leu Ile
            195                 200                 205

Asn Glu Pro Arg Cys Gln Val Asp Phe Ser Gly Lys Thr Leu Asn Ala
    210                 215                 220

Trp Val Gln Glu Met Ala Thr Tyr Val Lys Ser Leu Asp Asn Lys His
225                 230                 235                 240

Leu Leu Glu Ile Gly Met Glu Gly Phe Tyr Gly Asp Ser Met Pro Gly
                245                 250                 255

Lys Lys Gln Tyr Asn Pro Gly Tyr Gln Val Gly Thr Asp Phe Ile Thr
                260                 265                 270

Asn Asn Leu Ile Lys Glu Ile Asp Phe Ala Thr Ile His Ala Tyr Pro
            275                 280                 285

Asp Ile Trp Leu Ser Gly Gln Ser Asp Gly Ala Gln Met Met Phe Met
    290                 295                 300

Arg Arg Trp Met Thr Ser His Ser Thr Asp Ser Lys Thr Ile Leu Lys
305                 310                 315                 320

Lys Pro Leu Val Leu Ala Glu Phe Gly Lys Ser Ser Lys Asp Pro Gly
                325                 330                 335
```

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```
Tyr Ser Leu Tyr Ala Arg Glu Ser Phe Met Ala Ala Ile Tyr Gly Asp
            340                 345                 350
Ile Tyr Arg Phe Ala Arg Arg Gly Gly Ile Ala Gly Gly Leu Val Trp
            355                 360                 365
Gln Ile Leu Ala Glu Gly Met Gln Pro Tyr Ala Asp Gly Tyr Glu Ile
        370                 375                 380
Val Leu Ser Gln Asn Pro Ser Thr Gly Arg Ile Ile Ser Gln Gln Ser
385                 390                 395                 400
Arg Gln Met Thr Ser Leu Asp His Met Ser Ser Asn Arg Thr Asn Ser
            405                 410                 415
Gln Ser Asn Lys Leu Arg Asn Ser Lys Glu Gln
            420                 425
```

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGNATGGARG GNTTYTAYGG   20

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTTTTTTTTT TTTTT   15

(2) INFORMATION FOR SEQ ID NO: 5:

  (i) SEQUENCE CHARACTERISTICS:

   (A) LENGTH: 17 base pairs

   (B) TYPE: nucleotide

   (C) STRANDEDNESS: single

   (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: other nucleic acid

   (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAATCTGTGC CCACTTG   17

(2) INFORMATION FOR SEQ ID NO: 6:

  (i) SEQUENCE CHARACTERISTICS:

   (A) LENGTH: 17 base pairs

   (B) TYPE: nucleotide

   (C) STRANDEDNESS: single

   (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: other nucleic acid

   (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GTAAAACGAC GGCCAGT   17

(2) INFORMATION FOR SEQ ID NO: 7:

  (i) SEQUENCE CHARACTERISTICS:

   (A) LENGTH: 17 base pairs

   (B) TYPE: nucleotide

   (C) STRANDEDNESS: single

   (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: other nucleic acid

   (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGAAACAG CTATGAC   17

(2) INFORMATION FOR SEQ ID NO: 8:

  (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 21 amino acids

             (B) TYPE: amino acid

             (C) STRANDEDNESS: [lacuna]

             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ser Phe Asn Phe Val Lys Thr Arg Gly Thr Glu Phe Val Met Asp Xaa
1   5   10   15

Arg Phe Leu Tyr Leu
            20

(2) INFORMATION FOR SEQ ID NO: 9:

        (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 10 amino acids

             (B) TYPE: amino acid

             (C) STRANDEDNESS: [lacuna]

             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

             Thr Trp Ala Phe Ser Asp Gly Gly Tyr Arg
             1   5   10

(2) INFORMATION FOR SEQ ID NO: 10:

        (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 17 amino acids

             (B) TYPE: amino acid

             (C) STRANDEDNESS: [lacuna]

             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Glu Tyr Asn Pro Gly Tyr Gln Val Gly Thr Asp Phe Ile Ser Asn Asn
1               5                   10                      15
```

Arg

(2) INFORMATION FOR SEQ ID NO: 11:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 36 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTCTTATCCC TGGATCCCGA AAATCATATA GTTTCT   36

(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 40 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTACTCTGCA GACTTTCTGG AAGACTGATC ACTGCTCCTT   40